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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                     Database
                                                                                                                                             Post-processing: Listing first 45
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                             Scoring table:
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seq length:
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                                                                                                                                                                                                                                                                                                                                                                                                                  December 27, 2004, 17:02:30 ; Search time 66.75 Seconds (without alignments) 37.620 Million cell updates/sec
                                                                                                                                                                                                                                                                                  2002273 seqs, 358729299 residues
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                                                                                                                A_Geneseq_23Sep04:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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Zinc fing		VEC	VEG	VEG	VE(fing	fing	puti	fing	fine	fing	fine	fine	Suti							

ALIGNMENTS

RESULT 1 AAB84241 ID AAB8 Case CC, 06-DEC-1999; 07-JUN-2001. Synthetic. cardiovascular disease; diabetes. Phenotype associated gene; zinc finger protein; cancer; nephritis; prostate hypertrophy; hematopoiesis; osteoporosis; obesity; Zinc protein recognition helix SBS9 for target DNA triplet GAC. AAB84241; 06-DEC-2000; 2000WO-US033086. WO200140798-A2. 06-AUG-2001 AAB84241 standard; peptide; 7 (SANG-) SANGAMO BIOSCIENCES INC Liu Q, (first entry) 99US-00456100. Rebar EJ; Æ

Identifying genes associated with selected phenotype for research purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected phenotype.

WPI; 2001-374953/39

Example 1; Page 36; 58pp; English.

The specification describes a method for identifying genes associated with a selected phenotype. The method involves providing a library of nucleotide sequences encoding partially randomized zinc finger proteins, transducing cells with expression vectors, each comprising a sequence from the library, culturing the cells for expressing the zinc finger protein, assaying the cells for selected phenotype, and identifying the gene of interest, in cells exhibiting the phenotype. The method is useful for identifying a gene or genes associated with a selected phenotype such as the one related to cancer, nephritis, prostate hypertrophy, hematopoiesis, osteoporosis, obesity, cardiovascular disease or diabetes. The method is useful in academic laboratories, in the biotechnological industries, and in pharmaceutical, genomic, agricultural

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                           CC functional domain; and contacting the regulatory molecule with the cell.

CC The method is used for regulating the expression of a gene (e.g., a gene cencoding a nuclear receptor such as estrogen receptor alpha (ERalpha), cc estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha continued and contact factor 4 alpha continued and contin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to regulating the expression of a gene resthe chromatin of a cell. The method involves identifying one or accessible regions in cellular chromatin associated with gene; carrelated accessions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulating expression of gene by contacting cell with regulatory molecule comprising DNA-binding domain targeted to sequence within accessible region of cellular chromatin associated with a gene, and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a regulatory molecule, where the regulatory molecule comprises a DNA-
binding domain targeted to a sequence within the accessible region, and a
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neuroprotective;
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7; Conservative
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antirheumatic; antiarthritic; antipsoriatic; nootropic;
cerebroprotective; estrogen receptor alpha; ER-alpha;
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                                                                                                                                                                                                                              Regulating expression of gene by contacting cell with regulatory molecule comprising DNA-binding domain targeted to sequence within accessible region of cellular chromatin associated with a gene, and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression;
neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                     Wolffe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ER-alpha locus targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         research of both nuclear receptors of known function as well as thos
unknown function. The method also facilitates development of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200244386-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZFP; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUTZ
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antidiabetic; ophthalmological; vasotropic; chromatin;
antirheumatic; antiarthritic; antipsoriatic; nootropic
cerebroprotective; estrogen receptor alpha; ER-alpha;
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                                                                                                                                                                                                                                                                                                    Collingwood T;
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Pred. No.
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the chromatin of a cell The method involves identifying one or more accessible regions in cellular chromatin associated with gene; designing a regulatory molecule, where the regulatory molecule comprises a DNA-binding domain targeted to a sequence within the accessible region, and a functional domain; and contacting the regulatory molecule with the cell. The method is used for regulating the expression of a gene (e.g., a gene encoding a nuclear receptor such as estrogen receptor alpha (ERalpha), estrogen receptor beta (ERbeta), heparcoyte nuclear factor 4 alpha (HNF4alpha), heparcoyte nuclear factor 4 gamma (HNF4gamma), peroxisome proliferator activated receptor gamma (FPARgamma), retinoid x receptor alpha (RXRalpha), or constitutively active receptor alpha (CARalpha)) residing in the chromatin of a cell. Regulation of gene expression (such as nuclear receptor genes) will be useful in treatment of various diseases, including cancer, diabetes and cardiovascular disease, where

Example 1;

Page

44;

64pp;

English.

invention relates to regulating chromatin of a cell. The method

the expression of a gene

residing in

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RESULT 4
ABPSO162
ID ABPS
XX ABPS
AC ABPS
XX Zinc
XX WPI
XX (SA)
XX WPI
XX CC
XIN
CCC LTAR
CCC LTAR
CCC Sin
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (N); (2) a polypucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, thus designing (I) that binds to a target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the same target subsites to a target subsite (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carry out the regulation. The method is also useful for modulation of gene expression for therapeutic or prophylactic applications e.g., diabetic retinopathy, ischaemia, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's disease, stroke, etc. The method also has applications in pharmaceutical research of both nuclear receptors of known function as well as those of unknown function. The method also facilitates development of tissue and animal models of disease states, drug validation, and therapeutic product development. The methods also allow identification of the role of nuclear receptors of unknown functions in cellular homeostasis. Sequences ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that were fused to functional domains and tested for their ability to regulate expression of the ER in living cells
                                                                                                                                                                                                                                                                                                                                                                                                                    New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, compr first, second and third zinc fingers, ordered from N- to C-terminus.
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                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 57; 81pp; English.
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7; Conserv
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Pred. No.
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The present invention describes a zinc finger protein (I) that binds to a CC target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (1) a polypeptide (CC (II) comprising (I); (2) a polymcleotide (III) encoding (I) or (III); and (CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it CC that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it could be selected to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (CC that it binds to the S3 target subsite, thus designing (I) that binds to complete site. (I) is useful for recognition of triplet target subsites (CC useful in studying gene function, and for human therapeutics and plant condulate the expression of a target region within a subject, in the CC diagnostic methods to condulate the expression of a target region within a subject, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
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7; Conserva
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Pred. No. 1.7e+06;
Mismatches 0;
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RESULT 6
ABP51092
CC target site, comprising a first (F1), a second (F2), and a third (F3) (C zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC target site comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (1) a polypeptide (CI) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (C (3) designing (M) (I) involves selecting the F1 zinc finger such that it CC binds to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S1 target subsite, and selecting the F3 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, thus designing (I) that binds to the T2 zinc (I) is useful for recognition of triplet target subsites (I) is constituted in studying gene function, and for human therapeutics and plant (2) constituted the expression of a target region within a subject, in (2) condulate the expression of a target region within a subject, in (3) has improved affility and specificity for their carget sequences, as well as enhanced biological activity. AB071213 to AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene function
first, second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger protein that binds to target site, gene function and for human therapeutics and plant first, second and third zinc fingers, ordered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present inverting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a zinc finger protein (I) that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 63; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-500284/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2000; 2000US-00716637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc finger protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger protein related peptide motif SEQ ID NO:3976.
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRSNLTR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZFP; DNA binding protein; zinc finger
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       red. No. 1.7e+06;
Mismatches 0;
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                                                                                                                                      The present invention describes a zinc finger protein (I) that binds to a CC target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and CC (II) comprising (M) (I) involves selecting the F1 zinc finger such that it to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F2 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, and selecting the F3 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, and selecting the F2 zinc finger such that it CC useful in studying gene function, and for human therapeutics and plant CC diagnostic methods for sequence specific detection of target mucleic acid cin a sample, and in assays to determined the phenotype and function of CC used target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51330 represent DNA target sequences and zinc CC ABQ72214 and ABP48191 to ABP51330 represent DNA target sequences and zinc CC sequences and cannot be accomplished to the processor of the consent the sequences and zinc consent the sequences an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprifirst, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc finger protein related peptide motif SEQ ID NO:2791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2000; 2000US-00716637
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Pred. No.
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                                                                                                                  the exemplification
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RESULT 8
ABP49313
ADP49313
ADP7 20-A
ADPA 20-A

                                                                                                                                                                                                                                               cc target site, comprising a first (F1), a second (F2), and a third (F3) cz zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the Ct target site comprises, in 3'-5' direction, a first (S1), a second (S2), cc and a third (S3) target subsite. Also described are: (1) a polypeptide (CI) comprising (I); (2) a polynucleotide (II) encoding (I) or (II); and (CI) designing (M) (I) involves selecting the F2 zinc finger such that it (CI) binds to the S1 target subsite, and selecting the F3 zinc finger such that it (CI) to the S2 target subsite, and selecting the F3 zinc finger such that it (CI) to the S3 target subsite, and selecting the F3 zinc finger such that it (CI) is useful for recognition of triplet target subsites that it binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to complete the comprise of the subsites of the subsite of the subsites of the subsite of the subsit
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Query Match 100.0%; (Best Local Similarity 100.0%; )
Matches 7; Conservative 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, compr first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-500284/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a zinc finger protein (I) that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 48; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu Q;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
Score 7; DB 5; Le
Pred. No. 1.7e+06;
); Mismatches 0;
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Pred. No. 1.7e+06;
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                                                                         Length 7;
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   Indels
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Ş 밁

DRSNLTR

Matches

7; Conservative Similarity

100.0%;

0;

Mismatches

Indels

0

Gaps

0

1.7e+06 <u>,,</u>

Local

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RESULT 9
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                                                                                                                                  The present invention describes a zinc finger protein (I) that binds to a carget site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the care target site comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (C) dinds to the S1 target subsite, selecting the F1 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to ca target site. (I) is useful for recognition of triplet target subsites. (CC a target site. (I) is useful for recognition of triplet target subsites. (I) is conditate the expression of a target region within a subject, in caption of the subsite of captions of the subsite. (I) is sufficiently and specificity for their conditate the expression. (I) has improved affinity and specificity for their caption of the subsite subsite. (I) has improved affinity and specificity for their caption of the subsite subsite. (I) has improved affinity and specificity for their caption of the subsite. (I) as enhanced biological activity. ABQ71213 to caption of the subsite. (I) as supplementation of the present DNA target sequences and zinc finger particles and zinc finger protein subsite.
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprifirst, second and third zinc fingers, ordered from N- to C-terminus.
                                                             Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-500284/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 57; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu 0,
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                                                                                                    finger peptides which are given in the exemplification of the present invention
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                     100.0%;
Score 7;
Pred. No.
                     DB 5;
                     Length 7;
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RESULT 10 ABP50373

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RESULT 11
ABP48386
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                                                                                                                                                                                                                                                                                                CC target site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it comprise to the S1 target subsite, selecting the F2 zinc finger such that it comprise to the S2 target subsite, and selecting the F3 zinc finger such that it thinds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (C a target such that it or the subsite of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant CC engineering. (I), (II) or (III) is useful in therapeutic methods to CC diagnostic methods for sequence specific detection of target nucleic acid con a sample, and in assays to determined the phenotype and function of CC gene expression. (I) has improved affinity and specificity for their CC target sequences, as well as enhanced biological activity. AB071213 to 10 (2) invention.

CC finger peptides which are given in the exemplification of the present convertion.
                                                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                               Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu Q;
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                                                                                                                           DRSNLTR 7
                                                                                                                                                                 Conservative
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                                                                                                                                                                 100.0%; Score 7; DB
100.0%; Pred. No. 1.
tive 0; Mismatches
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1.7e+06;
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RESULT 12
ABP49231
ID ABP49
XX
AC ABP49
XX

ABP49231 standard; peptide;

0

ABP49231;

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polypuclectide (III) encoding (I) or (II); and (S3) target subsite, and selecting the F1 zinc finger such that it comprises to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target subsite to recognition of triplet target subsites (I) is useful for recognition of the subsite. (I) is useful for recognition of the subsite. (I) is useful in studying gene function, and for human therapeutic sand plant (C) engineering. (I), (II) or (III) is useful in therapeutic methods to (C) diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc invertion.
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                              á
                                                                                Query Match
Best Local S
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, compr first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                     Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 37; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger protein; ZFP; DNA binding protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein related peptide motif SEQ ID NO:395.
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                   1 DRSNLTR
                                                                Similarity 7; Conserv
                                                                                                                                      AA;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                  100.0%;
                                                                    0;
                                                                                    Score 7;
Pred. No.
                                                                      Mismatches
                                                                                    DB 5; Le
                                                                                                    Length 7;
                                                                      Indels
                                                                      0;
                                                                      Gaps
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28-AUG-2002

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RESULT 13
ABP49241
SEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC target site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus; where the CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus; where the CC target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polypucleotide (III) encoding (I) or (II); and (C) designing (M) (I) involves selecting the F1 zinc finger such that it CC binds to the S1 target subsite, and selecting the F3 zinc finger such that it CC binds to the S2 target subsite, and selecting the F3 zinc finger such that it could be considered to the S2 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (C) that it binds to the S3 target subsite, but designing (I) that binds to constitute the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant (C) modulate the expression of a target region within a subject, in (C) diagnostic methods for sequence specific detection of target nucleic acid (C) in a sample, and in assays to determined the phenotype and function of C) and constitute the constitute of their constitute such as well as enhanced biological activity. AB071213 to (C) invention of the present (C) in the constitute (C) in the present (C) i
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                  Zinc finger protein related peptide motif SEQ ID NO:1553.
                                                               28-AUG-2002
                                                                                                         ABP49241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                 ABP49241 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-500284/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc finger protein; ZFP; DNA binding protein; zinc finger
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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Page 48; 81pp; English.
                                                                                                                                                                                                                                                                                              DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB
100.0%; Pred. No. 1:
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   BB
                                                                                                                                                                                                                                                                                                                                                                                1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
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RESULT 14
ABP49259
ID ABP49259
XX ABP45
XX ABP45
XX ABP45
XX ZAP45
XX ZAP45
XX Zinc
XX Zinc
XX Zinc
XX Zinc
XX Zinc
XX Homo
OS Homo
OS Synth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC The present invention describes a zinc finger protein (I) that binds to a CC target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polypucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F3 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, and selecting the F3 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to constitute the side of the S3 target subsite, thus designing (I) that binds to CC useful in studying gene function, and for human therapeutics and plant CC engineering. (I), (II) or (III) is useful in therapeutic methods to CC modulate the expression of a target region within a subject, in CC diagnostic methods for sequence specific detection of target nucleic acid con a sample, and in assays to determined the phenotype and function of CC gene expression. (I) has improved affinity and specificity for their CC target sequences, as well as enhanced biological activity. AB071213 to invention of the persent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                              Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7
  Synthetic
                        Homo sapiens
                                                                                                      Zinc finger
                                                                                                                                                   28-AUG-2002
                                                                                                                                                                                                                                      ABP49259 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              finger peptides which invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 48; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, compr first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2000; 2000US-00716637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2001; 2001WO-US043438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                            1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                       1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 5; Le ilarity 100.0%; Pred. No. 1.7e+06; Conservative 0; Mismatches 0;
                                                              protein;
                                                                                                        protein related peptide motif SEQ ID NO:1559.
                                                                                                                                                   (first entry)
                                                              ZFP; DNA binding protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ABP49880
ID ABP49
XX ABP49
AC ABP49
XX ABP49
XX Zinc
DE Zinc
XX Zinc
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a zinc finger protein (I) that binds to a crarget site, comprising a first (F1), a second (F2), and a third (F3) (Z zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the cand a third (S3) target subsite. Also described are: (1) a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polymucleotide (III) encoding (I) or (II); and (S3) target subsite. Also described are: (1) a polypeptide (S3) designing (M) (I) involves selecting the F1 zinc finger such that it (C) binds to the S1 target subsite, selecting the F2 zinc finger such that it thinds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target subsite of the recognition of triplet target subsites (I) is useful for recognition of triplet target subsites (I) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in (C) diagnostic methods for sequence specific detection of target nucleic acid (I) a sample, and in assays to determined the phenotype and function of construction (I) has improved affinity and specificity for their (C) and (C) a
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Best Local
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                                                                                                                                                                                                                                                                                  Zinc finger protein;
                                                                                                                                                                                                                                                                                                                                                           Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 48; 81pp; English.
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            30-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP49880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP49880 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                               protein related peptide motif SEQ ID NO:3572.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 5; Lengtn /; 100.0%; Pred. No. 1.7e+06; 100.0%; O. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  ZFP; DNA binding protein; zinc finger
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Search completed: December 27, 2004, 18:06:44 Job time : 67.75 secs

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DRSNLTR

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The present invention describes a zinc finger protein (I) that binds to a crinc finger, comprising a first (F1), a second (F2), and a third (F3) cz inc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the crince site comprises, in 3'-5' direction, a first (S1), a second (S2), cz and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polypuncleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it to the S2 target subsite, and selecting the F3 zinc finger such that it to the S2 target subsite, and selecting the F3 zinc finger such that it compared to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) is useful in studying gene function, and for human therapeutic and plant condulate the expression of a target position of the subsite. (I) is useful in therapeutic methods to condulate the expression of a target region within a subject, in condulate the expression of a target region within a subject, in condulate the subsite of a sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of CC abd72214 and AbP48191 to AbP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present convention.
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                                                       Matches
                                                                           Best
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                               Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 55; 81pp; English.
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                                                                           Local
     1 DRSNLTR 7
                                                    Similarity 7; Conserv
                                                                                                                                                    A
                                                       Conservative
                                                    100.0%; Score 7; DB
100.0%; Pred. No. 1.7
tive 0; Mismatches
                                                                             DB 5; Lo
                                                                                                    Length 7;
                                                         Indels
                                                         0
                                                         Gaps
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Patent No. 6503/1,
Papelicant: Liu, Qiang
Applicant: Liu, Qiang
Applicant: Rebar, Edward J.
Applicant: Rebar, Edward J.
Applicant: Sangamo Bioscience, Inc.
Applicant: Sangamo Bioscience, Inc.
PITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
PITLE OF INVENTION: Proteins for the Identification of Gene Function
PILE REFERENCE: 0.19496-003210US
PILE REFERENCE: 0.19496-003210US
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR PILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-731-558-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09731558 Patent No. 6503717
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seq length: 2000000000
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Match Length
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| Compared_Patents_AA:*
| Compared_Patents_ACOMB.pep:*
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US-09-424-487B-11
US-08-793-408-18
US-09-139-762A-18
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Sequence
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APPLICANT: CHOO, YEN
APPLICANT: KLJG, AARON
APPLICANT: KLJG, AARON
APPLICANT: ISALAN, MARK
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: GB 9710809.6
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1998-05-26
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
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US-08-793-408-18
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HENGTH: 27
TYPE: PRT
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Matches 7; Conserval
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LENGTH: 7
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                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating
TITLE OF INVENTION: Binding Proteins for Recogni
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                                                                                                                    NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                 STREET: 1100 New CITY: Washington STATE: D.C.
                             COUNTRY:
                                                                                   ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W.
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                  20005-3918
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100.0%; Pred. No. 3.1
tive 0; Mismatches
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Pred. No. 0.064;
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect

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RESULT 4
US-09-139-762A-18
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APPLICATION NUMBER: US/09/139,762A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-UUL-1995
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/793,408
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
IITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 94
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
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Query Match
Best Local Similarity
""" Conserve
Search completed: December 27, 2004, 18:12:04 Job time : 16.8 secs
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APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-00V-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                    TOPOLOGY: un
                                                                                                                                                                                                                             LENGTH: 89 amino acids
TYPE: amino acid
                                                         74 DRSNLTR
                                                                                    1 DRSNLTR 7
                                                                                                                Conservative
                                                                                                                                                                                                    unknown
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                                                                                                                             100.0%; Score 7;
100.0%; Pred. No.
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Result
No.
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US-09-731-558-13
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09731558 Patent No. 6503717
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 7
                                                  APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: OF O19946-003210US
FILE REFERENCE: 019496-003210US
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
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Match Length
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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Sequence 43, Appl
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Search completed: December 27, 2004, 18:12:03 Job time : 15.8 secs
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                                                                                                                                                                                                                                             APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 43
LENGTH: 7
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Patent No. 6689558
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ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Description OTHER INFORMATION: recognition
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GenCore version Copyright (c) 1993 - 2004

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Database :
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SUMMARIES

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RESULT 1 AAE08727 ID AAE0 Human KCA4 protein F1 recognition helix. 15-NOV-2001 (first entry) AAE08727; AAE08727 standard; peptide; 7 A

Human; KCA4; EPO; molecular target; zinc finger protein; ZFP; cellular process; signal transduction; drug-screening.

Homo sapiens.

WO200159450-A2

16-AUG-2001.

08-FEB-2001; 2001WO-US004301.

08-FEB-2000; 2000US-0181117P.

(SANG-) SANGAMO BIOSCIENCES INC.

WPI; 2001-522491/57.

Case C;

Screening compound for interaction with molecular target by contacting compound with cells, comprising exogenous zinc finger protein that modulates expression of target, and determining values of properties of

Example 10; Page 73; 99pp; English.

The invention relates to a method of screening a compound for interaction with a molecular target. The method involves contacting first and second cells with the compound and determining the values of properties of the compound. The second cell comprises an exogenous zinc finger protein (ZFP) that modulates the expression of the molecular target, or isolating membranes from cell comprising ZFP. The methods allow for high throughput screening of candidate compound and reduces the incidence of false positives. The methods are useful for screening a compound for interaction with a molecular target or for screening a compound for its capacity to transduce a signal to the molecular target or its capacity to block transduction of a signal through the molecular target,

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RESULT 2
ABB807992
ID ABB8
XX AAC ABB8
XX 
                                                                                          The invention relates to regulating the expression of a gene residing in the chromatin of a cell. The method involves identifying one or more accessible regions in cellular chromatin associated with gene; designing a regulatory molecule, where the regulatory molecule comprises a DNA-binding domain targeted to a sequence within the accessible region, and a functional domain; and contacting the regulatory molecule with the cell. The method is used for regulating the expression of a gene (e.g., a gene encoding a nuclear receptor such as estrogen receptor alpha (ERalpha), eastrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha (ERF4alpha), hepatocyte nuclear factor 4 alpha (ERF4alpha), hepatocyte nuclear factor 4 pamma (HNF4gamma), peroxisome proliferator activated receptor gamma (FPARgamma), retinoid X receptor alpha (EXRalpha), or constitutively active receptor alpha (CARalpha)) residing in the chromatin of a cell. Regulation of gene expression (such as nuclear receptor genes) will be useful in treatment of various disease, including cancer, diabetes and cardiovascular disease, where the regulatory molecule as described above, is contacted with the cell to carry out the regulation. The method is also useful for modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 7
   gene expression for therapeutic or prophylactic applications e.g. diabetic retinopathy, ischaemia, macular degeneration, rheumatoic arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SANG-) SANGAMO BIOSCIENCES INC.
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antirheumatic; antiarthritic; antipsoriatic; nootropic
cerebroprotective; estrogen receptor alpha; ER-alpha;
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J. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antianaemic; neuroprotective; nootropic; cerebroprotective; antiinflammatory; antiinflammatory; antiinflammatory; cardiant; immunosuppressive; tumour metastasis; inflammatory disease; allograft rejection; cell migration; angiogenesis; basement membrane; extracellular matrix; cancer; ischaemia; diabetic retinopathy; macular degeneration; rheumatoid arthritis; psoriasis; HUV infection; sickle cell anaemia; Alzheimer's disease; muscular dystrophy; neurodegenerative disease; vascular disease; cardiovascular disease;
                                                                                                                                                  The invention relates to novel heparanase sequences, particularly novel sequences from the regulatory regions upstream and downstream of the coding region. The activity of polynucleotides of the invention may be described as, cytostatic, vasotropic, antidiabetic, anti-HIV, ophthalmological, antirheumatic, antiarthritic, antipsoriatic, antiarement manufacture anti-mentic control of the invention of the invention of the invention may be described as cytostatic, vasotropic, antidiabetic, anti-HIV, ophthalmological, anti-neumatic, anti-mentic, anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-527708/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Page 49;
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hes 0;
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antianaemic, neuroprotective, nootropic, ce antibacterial, virucide, protozoacide, fung cardiant and immunosuppressive. Modulating using constructs of the invention is useful

invention is useful

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antianaemic; neuroprotective; nootropic; cerebroprotective; antianaemic; neuroprotective; motoroacide, fungicide; antiinflammatory; cardiant; immunosuppressive; tumour metastasis; inflammatory disease; allograft rejection; cell migration; angiogenesis; basement membrane; extracellular matrix; cancer; ischaemia; diabetic retinopathy; macular degeneration; rheumatoid arthritis; psoriasis; HIV infection; sickle cell anaemia; Alzheimer's disease; muscular dystrophy; neurodegenerative disease; vascular disease; cardiovascular disease; cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.
                 The invention relates to novel heparanase sequences, particularly novel sequences from the regulatory regions upstream and downstream of the coding region. The activity of polynucleotides of the invention may be described as, cytostatic, vasotropic, antidiabetic, anti-HIV,
                                                                                                                                                                New heparanase polynucleotide, useful for controlling disease states such as tumor metastasis, inflammatory diseases and allograft rejection.
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polypucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extracellular matrix. Hepatranase-targeted DNA binding domains modulates gene expression, and are useful for therapeutic or prophylactic applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative diseases, vascular disease, cardiovascular disease, cystic fibrosis, stroke, and bacterial, protozoal, fungal and viral infection. Constructs of the invention may also be useful in gene therapy. The current sequence represents a finger of a three-finger ZFP (zinc finger protein), which has a target site in the human heparanase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antianaemic, neuroprotective, nootropic, cerebroprotective, antibacterial, virucide, protozoacide, fungicide, antiinflammatory, antibacterial, virucide, protozoacide, fungicide, antiinflammatory, cardiant and immunosuppressive. Modulating expression of heparanase gene using constructs of the invention is useful for facilitating targeted control of disease states such as tumour metastasis, inflammatory diseases, allograft rejection, and for inhibiting processes such as cell migration, angiogenesis, and degradation of the basement membrane and/or
                                                                                                                                                                                                                                            New zinc finger protein that binds to target site, gene function and for human therapeutics and plant first, second and third zinc fingers, ordered from
                                                                                                                                                                                                        Example 1; Page 54; 81pp;
                                                                                                                                                                                                                                                                                                                              WPI; 2002-500284/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2001; 2001WO-US043438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc finger protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc finger protein related peptide motif SEQ ID NO:2534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP49764 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2000; 2000US-00716637.
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                                                                                                                                                                                                                                                                                                                                                                                                              (SANG-) SANGAMO BIOSCIENCES INC
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                                                                                                                                                                                                      English
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Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                engineering, comp
N- to C-terminus.
                                                                                                                                                                                                                                                                                        useful in studying
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RESULT 6
ABP50067
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XX ABP5
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Matches
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the sate of the S3 target subsite, thus designing (I) that binds to the sate of the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S4 target subsite, thus designing (I) that binds to the S4 target subsite, thus designing (I) that binds to the S4 target subsite, thus designing (I) that binds to the S4 target subsite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site, gene function and for human therapeutics and plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc finger protein; ZFP; DNA binding protein; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSDHLAR
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100.0%; Pred. No.
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N- to C-terminus.
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The present invention describes a zinc finger protein (I) that binds to a comparish comprising a first (FI), as second (F2), and a third (F3) comprised FI, F2, F3 from N-terminus to C-terminus, where the CC target site comprises, in 3'-5' direction, a first (S1), a second (S2), comprising (I); (2) a polymucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it cC binds to the S1 target subsite, selecting the F2 zinc finger such that it cC binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it cC binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, thus designing (I) that binds to ca target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such cC ca target site. (I) is useful for recognition of triplet target subsites (I) is constituted in studying gene function, and for human therapeutics and plant constitute the expression of a target region within a subject, in cc diagnostic methods for sequence specific detection of target nucleic acid cin a sample, and in assays to determined the phenotype and function of
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                          New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprifirst, second and third zinc fingers, ordered from N- to C-terminus.
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Pred. No. 1.7
); Mismatches
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1.7e+06;
hes 0;
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RESULT 8
ABP48652
ID ABP4
AC A
CC target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC zinc finger subrites, in 3-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (III) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (C) designing (M) (I) involves selecting the F1 zinc finger such that it (C) binds to the S1 target subsite, selecting the F2 zinc finger such that it (C) binds to the S2 target subsite, and selecting the F3 zinc finger such that it (C) that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (C) that it binds to the S3 target subsite, thus designing (I) that binds to constitute the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant (C) the constant of a target region within a subject, in (C) diagnostic methods for sequence specific detection of target nucleic acid (C) in a sample, and in assays to determined the phenotype and function of (C) see the sequences, as well as enhanced biological activity, AB071213 to (C) AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc (C) finger peptides which are given in the exemplification of the present
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-500284/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu Q
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invention
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Pred. No.
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RESULT 9
ABP49518
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                                              CC target site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC target site comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it common to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F3 zinc finger such that it common to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to catarget site. (I) is useful for recognition of triplet target subsites (I) is useful in studying gene function, and for human therapeutics and plant CC diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of CC target sequences, as well as enhanced biological activity. ABO71213 to CC target and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprifirst, second and third zinc fingers, ordered from N- to C-terminus.
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                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a zinc finger protein (I) that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 51; 81pp; English
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                                   finger peptides which invention
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Pred. No. 1.7
0; Mismatches
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Sequence 7

Length 7;

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Query Match
Best Local Similarity
"---hes 7; Conserve
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                                                                                                                                                                                        The present invention describes a zinc finger protein (I) that binds to a carget site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the zinc finger ordered F1, F2, F3 from N-terminus to C-terminus, where the comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (C1) comprising (I); (2) a polymuclectide (III) encoding (I) or (II); and (C3) designing (M) (I) involves selecting the F1 zinc finger such that it composed to the S1 target subsite, selecting the F2 zinc finger such that it (C2) binds to the S2 target subsite, and selecting the F3 zinc finger such that it composed to the S3 target subsite, and selecting the F3 zinc finger such that it composed to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to cataget site. (I) is useful for recognition of triplet target subsites (C1) is useful in studying gene function, and for human therapeutics and plant (C2 engineering (I), (II) or (III) is useful in therapeutic methods to composed for human therapeutic methods to composed for sequence specific detection of target nucleic acid cataget sequences, as well as enhanced biological activity. ABO71213 to absolute the subsite of the subsite of target sequences, as well as enhanced biological activity. ABO71213 to absolute the subsite of target sequences, as well as enhanced biological activity.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                      ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention
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                                                                                               Sequence 7
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                    Conservative
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
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100.0%; Pred. No.
tive 0; Mismatc
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RESULT 11
ABP48
AC AB
                                                                                                                                                                                                                                                                                                                                    The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the cand a third (S3) target subsite. Also described are: (I) a second (S2), cand a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (S) designing (M) (I) involves selecting the F1 zinc finger such that it (S) inds to the S1 target subsite, and selecting the F2 zinc finger such that it (S) binds to the S2 target subsite, and selecting the F3 zinc finger such that it (S) in the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target subsite, and selecting the F3 zinc finger such that it (S) is useful for recognition of triplet target subsites (I) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in (C) diagnostic methods for sequence specific detection of target nucleic acid (S) a sample, and in assays to determined the phenotype and function of (S) and (S) as well as enhanced biological activity. ABQ71213 to (B) in the S) are sequences and zinc (S) invention of the present (S) invention (S) in the (S) 
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                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
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                                                                                                                                                                                                                                          Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 41; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-500284/53
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    1 RSDHLAR 7
                                                                              Similarity 7; Conserv
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                                                                              100.0%; ilarity 100.0%; Conservative 0,
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                                                                                      <u>.</u>
                                                                                                                           Score 7;
Pred. No.
                                                                                      Mismatches
                                                                                                                                                                    DB 5;
                                                                                                                               1.7e+06;
                                                                                                                                                                Length 7;
                                                                                      Indels
                                                                                      0;
                                                                                      Gaps
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RESULT 12
ABP49260
ADP49260
ADP49260
ADP49260
AXX ABP49
AXX ABP49
AXX Zinc
XXX Zinc
XXX Zinc
XXX HOMMO
OS Synth
XX W0200
PD 30-MJ
XX Z0-NC
XX Z0-NC
AXX ISANC
XX ISAN
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                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                Sequence 7 AA;
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                                     RSDHLAR 7
                                                                                                                                            Conservative
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                                                                                                                                                                      100.0%; Score 7; DB 5; Lo
100.0%; Pred. No. 1.7e+06;
                                                                                                                                            0
                                                                                                                                            Mismatches
                                                                                                                                        0
                                                                                                                                                                                                        Length 7;
                                                                                                                                            Indels
                                                                                                                                    0,
                                                                                                                                    Gaps
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RESULT 13 ABP50082 ID ABP50082 standard; peptide; 7 AA.

RESULT 14 ABP48649

ABP48649 standard;

peptide; 7 AA.

28-AUG-2002 ABP48649;

(first entry)

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1 RSDHLAR 1 RSDHLAR

Matches Query Match Best Local

h 100.0%; Score 7; Similarity 100.0%; Pred. No. 7; Conservative 0; Mismatc

Mismatches

. 1.7e+06; ches 0; DB 5;

0

Gaps

0

Length 7; Indels

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CC target site, comprising a first (F1), a second (F2), and a third (F3) (C zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the CC target site comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (C) (3) designing (M) (I) involves selecting the F1 zinc finger such that it (C) binds to the S1 target subsite, selecting the F2 zinc finger such that it (C) binds to the S2 target subsite, and selecting the F3 zinc finger such that it (C) that it binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to carget site. (I) is useful for recognition of triplet target subsites (C) a target site. (I) is useful in studying gene function, and for human therapeutic methods to condulate the expression of a target region within a subject, in (C) diagnostic methods for sequence specific detection of target nucleic acid (C) in a sample, and in assays to determined the phenotype and function of CC sequences, as well as enhanced biological activity, AB071213 to (AB072214 and ABB48191 to ABP51230 represent DNA target sequences and zinc (C) invention.
Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                            finger peptides which invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 56; 81pp; English.
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  AA;
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RESULT 15
ABP49794
ID ABP49
XX ABP49
XX ABP49
XX ABP49
XX ABP49
XX ZB-AU
DT 28-AU
DX Zinc
XX Zinc
XX Zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a zinc finger protein (I) that binds to a carget site, comprising a first (F1), a second (F2), and a third (F3) CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the candidate comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polymucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it the condistance of the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the CC a target subsite, thus designing (I) that binds to a target subsite of the subsites of the subsite of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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       Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                                       Zinc finger protein related peptide motif SEQ ID NO:2544.
                                                                                                           28-AUG-2002
                                                                                                                                                                                                          ABP49794 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 
nes 7; Conserv
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                                                                                                        (first entry)
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Search completed: December 27, 2004, 18:06:43 Job time: 67.75 secs

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RSDHLAR 7

Matches

l Similarity 7; Conserva

Conservative

0;

Mismatches

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The present invention describes a zinc finger protein (I) that binds to a CC target site, comprising a first (FI), a second (F2), and a third (F3) CC zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger ordered FI, F2, F3 from N-terminus to C-terminus, where the CC zinc finger site comprises, in 3'-5' direction, a first (S1), a second (S2), CC and a third (S3) target subsite. Also described are: (I) a polypoptide (II) comprising (I), (2) a polypucleotide (III) encoding (I) or (II), and CC (II) designing (M) (I) involves selecting the F1 zinc finger such that it CC binds to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F2 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, and selecting the F2 zinc finger such that it CC that it binds to the S3 target subsite, thus designing (I) that binds to constitute the subsite of the subsite such that it construction of the subsite subsites (I) is useful for recognition of triplet target subsites (I) is useful in studying gene function, and for human therapeutics and plant CC engineering. (I), (II) or (III) is useful in therapeutic methods to cC diagnostic methods for sequence specific detection of target nucleic acid constituted to the expression. (I) has improved affinity and specificity for their CC target sequences, as well as enhanced biological activity. ABQ71213 to ABP32214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                       Sequence 7 AA;
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100.0%; Score 7;
100.0%; Pred. No.
DB 5; Li
1.7e+06;
                         Length 7;
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GENERAL INFORMATION:
APPLICANT: Case, Casey
ITITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regult
No.
OTHER INFORMATION:
OTHER INFORMATION:
US-09-779-233-42
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US-09-779-233-42
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Maximum DB
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                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09779233 Patent No. 6689558
                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                 LENGTH: 7
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Score Match Length DB
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                      Description of Artificial Sequence: recognition helix
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US-09-248-796A-16192
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Sequence 16192, A
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

ITITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

INUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16192

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-16192
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Search completed: December 27, Job time : 15.8 secs
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US-09-248-796A-16192
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Matches
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                                                                                                                                                                              Query Match
                                                                         57 RSDHLAR
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                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative 0
                                                                         63
                  2004, 18:12:03
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Pred. No. 0.23;
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Perfect score:
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Maximum DB seq length: 2000000000
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No matches found
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Score Match Length DB ID
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Gapop 60.0 , Gapext 60.0
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                                                                                              SUMMARIES
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                                                           Description
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Search completed: December 27, 2004, 21:40:38 Job time : 17.35 secs

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Retent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Goldberty, Brian A
APPLICANT: Goldberty, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
ITILE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
ITILE OF INVENTION: hoteropolyketide compounds
FILE REFERENCE: PCT/US 9/23535
CURRENT APPLICATION NUMBER: US/09/413,814
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US-09-413-814-44
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No.
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 60.0 , Gapext 60.0
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004
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29.289 Million cell updates/sec
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Compugen Ltd.
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Search completed: December 27, Job time: 16.85 secs
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                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 881
                                                                                                                             Query Match 100.0%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatci
                                                                                                                                                                                                         TYPE: PRT ORGANISM: Sorangium cellulosum
                                                                  295 RSDALAR 301
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                2004, 20:31:05
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Sequence 16, Application US/09731558

Sequence 16, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
ITILE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US 09/456,100

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16

LENGTH: 7
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No.
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US-09-731-558-16
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LENGTH: 7
TYPE: PRT
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SBS5
; OTHER INFORMATION: recognition helix
US-09-731-558-16

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 1 QSGSLTR 7
Db 1 QSGSLTR 7
Search completed: December 27, 2004, 20:31:04
Job time: 15.85 secs
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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq length: 2000000000
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No matches found
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                                                           Query
Score Match Length DB
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Search completed: December 27, 2004, 20:31:04 Job time : 15.85 secs

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                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-139-762A-19
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US-08-040-548-19
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US-08-620-151-111
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US-08-620-44-34
US-08-646-44-34
US-09-171-926-1
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US-09-710-37-1
US-09-710-37-1
US-09-710-37-1
US-09-710-37-1
US-09-716-337-1
US-09-716-337-1
US-09-229-007A-8
US-09-229-007A-8
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US-08-466-344-8
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TYPE: PRT
STREET: 1100
STREET: Mashington
CITY: Washington
                                                        NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P
STREET: 1100 New York Avenue, N.W.
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US-09-919-039-66	US-08-466-344-2	US-08-040-548-2	US-08-224-482-6	5206152-7	US-09-538-092-1278	US-08-224-482-8	US-09-500-700-44	US-08-676-318A-44	US-08-863-813A-44	US-09-500-700-36	US-09-500-700-34	US-08-676-318A-36	US-08-676-318A-34	US-08-863-813A-36	US-08-863-813A-34	US-08-224-482-11	US-09-500-700-5
66,	'n	Sequence 2, Appl:	Sequence 6, Appli	Patent No. 5206152	Sequence 1278, A	8, ,	-	Sequence 44, Appl	-	Sequence 36, App	•	Sequence 36, App	•	Sequence 36, App	34,	11,	Sequence 5, Appl

ALIGNMENTS

APPLICANT: CHOO, YEN APPLICANT: ISALAN, MARK APPLICANT: PATEL, SACHIN APPLICANT: HALASUBRAWANIAN, SHANKAR APPLICANT: LIU, XIAOHAI TITIE OF INVENTION: MOLECULES FILE REFERENCE: 71278/271599 CURRENT APPLICATION NUMBER: US/09/614,679A CURRENT FILING DATE: 2000-07-12 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTIN VEY. 2.1 SEQ ID NO 19 LENGTH: 7 Sequence 19, Application US/09139762A Patent No. 6013453 Sequence 19, Application US/09614679A Patent No. 6492117 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Choo, Yen APPLICANT: Klug, Aaron APPLICANT: Sanchez Garcia, Isidro APPLICANT: Sanchez Garcia, Isidro TITLE OF INVENTION: Improvements in or Relating to TITLE OF INVENTION: Binding Proteins for Recognition FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide ORGANISM: Artificial Sequence Similarity 7; Conserv Conservative 100.0%; 0; Pred. No. Score 7; Mismatches 3.8e+05; hes 0; DB 4; Length 7; Indels 0 Gaps

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of DNA

ZIP: 20005-3918 COMPUTER READABLE FORM:

COUNTRY: USA ZIP: 20005-3918

MEDIUM TYPE: COMPUTER: IE

Diskette

PC-DOS/MS-DOS

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Patent No. 6013453
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APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762.
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                 APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
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APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
                                                                                                                                                                                                                 ZIP: 20005-3918
COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                     US/09/139,762A
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Query Match
Best Local Similarity
"---hes 7; Conserv?
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                                                                                 US-08-040-548-19
                                                                                                                                                                                                APPLICATION NUMBER: US/08/040
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COUGHLIN, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd
TELECOMMUNICATION INFORMATION:
TELEPEAX: (312) 744-0090
TELEPEAX: (312) 744-090
TELEPEAX: (312) 745-4961
INFORMATION FOR SEQ ID NO: 19:
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Best Local Similarity luv.
""" hes 7; Conservative
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FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: GB 9514698.1
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FILING DATE: 17-AUG-1995
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                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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               Conservative
                                                                                                                    linear
                                                                                               peptide
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            100.0%; Score 7; DB
100.0%; Pred. No. 0.0
tive 0; Mismatches
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Pred. No.
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0.017;
                               DB 1; Length 20; 0.031;
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                 Indels
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RSDHLTT

RSDHLTT 15

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; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-344-19
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US-08-466-344-19
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                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                               Sequence 95, Application US/09229007A Patent No. 6453242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA: 08/040,548

APPLICATION NUMBER: 08/040,548

FILING DATE: 31-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Coughlin, Daniel F.

REGISTRATION NUMBER: 36,111

REFERENCE/DOCKET NUMBER: arcd067

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 744-0090
                                                           APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences,
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (312) 245-49
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentlIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: STREET: Chicago CITY: Chicago Illinois
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                                                                                                                                                                                                                                                                                                                                9
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321 No. 5773583th Clark Street, Suite 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245-4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Vikas P.
METHODS AND MATERIALS RELATING TO FUNCTIONAL DOMAINS OF DNA BINDING
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US-08-620-151-111
Sequence 11, Application US/08620151
Patent No. 5928955
GENERAL INFORMATION: APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
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Matches
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CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Patent No. 6785613
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
FILE REFERENCE: 019496-001800US
CURRENT EPPLICATION NUMBER: US/10/113,424
CURRENT FILING DATE: 2002-03-28
CURRENT FILING DATE: 1099-01-12
RIOR FILING DATE: 1999-01-12
RUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence OTHER INFORMATION: (F1, F2 and F3) from Zif 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             Local
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Conservative (
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llarity 100.0%;
Conservative 0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                           Score 7;
Pred. No.
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                                                                                                                                                                                                                                                                                                                           Mismatches
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ADDRESSEE:

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APPHLIANCE DATE:
CLASSIFICATION: 514
CTORREY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08040548 Patent No. 5763209
GENERAL INFORMATION:
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TELEFAX: 312-321-429
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sukhatme, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
                                                                                                                                                                                                                                                                                                                                    STREET: Chicago
CITY: Chicago
THATE: Illinois
TH.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/620,151 FILING DATE: 22-MAR-1996 CLASSIFICATION: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 85:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 100.0%; Score 7; DB 2;
Local Similarity 100.0%; Pred. No. 0.04;
hes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Shannon, Karen L. REGISTRATION NUMBER: 36,675
                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 60610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BRINKS, HOFER, GILSON & LIONE NBC Tower - Suite 3600, 455 N. Cityfront
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sukhatme, Vikas P.
SUKHATME, VIKAS P.
VENTION: METHODS AND MATERIALS RELATING TO THE VENTION OF DNA BINDING PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Query Match
Best Local Similarity
Thehes 7; Conserve
                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-466-344-34
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Best Local Similarity
Watches 7; Conserve
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                                                                                                                                                                                 TELEPHONE: (312) 744-0090
TELEPAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 34:
SEQUIENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08466344 Patent No. 5773583
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/040,548

FILING DATE: 31-MAR-1993

ATTORNEY/AGENT INPORMATION:

NAME: COUGhlin, Daniel F.

REGISTRATION NUMBER: 36,111

REFERENCE/DOCKET NUMBER: arcd067

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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APPLICANT: SUKhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 321 No.
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                              1 RSDHLTT 7
RSDHLTT 15
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321 No. 5773583th Clark Street, Suite 800
                                                                 Conservative
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                                                                                   100.0%; Score 7;
100.0%; Pred. No.
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100.0%; Pred. No.
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. 0.043;
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0.043;
                                                                                                 Length 28
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RESULT 11 US-09-058-459-1

Sequence 1, Applic Patent No. 6188965

Application US/09058459

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; SOFTWARE: Patent:
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: MOUSE
US-09-127-926-1
                                                                                                                                                                                                                                           TITLE OF INVENTION: Apparatus and Method for Automated Protein Design FILE REFERENCE: A65353-4/RFT/RMS/SJT
CURRENT APPLICATION NUMBER: US/09/127,926
CURRENT FILING DATE: 1998-07-31
PRIOR REFLICATION NUMBER: 60/043,464
PRIOR RILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-08-04
PRIOR APPLICATION NUMBER: 60/054,678
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-09-04
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
PRIOR APPLICATION NUMBER: 60/081,97
PRIOR APPLICATION NUMBER: 09/058,459
PRIOR APPLICATION NUMBER: 09/058,459
PRIOR APPLICATION NUMBER: 09/058,561
PRIOR APPLICATION NUMBER: 09/058,7561
PRIOR APPLICATION NUMBER: 09/058,7561
PRIOR APPLICATION NUMBER: 1998-06-01
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; TYPE: PRT
; ORGANISM: Mouse
US-09-058-459-1
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PRIOR FILING DATE: 1997-08
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-10
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 626931
                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Street, Art
APPLICANT: Su, Yaoying
TITLE OF INVENTION: App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                              Local Similarity hes 7; Conserv
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RSDHLTT 20
                               RSDHLTT 7
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Dahiyat, Bassil L.
Gordon, D. Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Street, Arthur
                                                              100.0%; Score 7; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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Pred. No. 0.043;
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                                                                             DB 3; Length 28; 0.043;
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GENERAL INFORMATION:
APPLICANT: Greisman, Harvey A.
APPLICANT: Greisman, Harvey A.
APPLICANT: Greisman, Harvey A.
APPLICANT: Pabo, Carl O.
APPLICANT: Massachusetts Institute of Technology
ITITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
ITITLE OF INVENTION: Finger Proteins for Diverse DNA Target Sites
FILE REFERENCE: 019496-000220US
CURRENT APPLICATION NUMBER: US/09/240,179
CURRENT PILING DATE: 1999-01-9
EARLIER APPLICATION NUMBER: US 60/073,223
EARLIER APPLICATION NUMBER: US 60/073,223
EARLIER FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 28
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CURRENT APPLICATION NUMBER: US/09/037,179B

CURRENT FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: US 08/102,942

PRIOR FILING DATE: 1993-08-02

PRIOR APPLICATION NUMBER: US 07/614,161

PRIOR PILING DATE: 1990-11-13

PRIOR PILING DATE: 1989-11-13

PRIOR FILING DATE: 1989-11-13
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US-09-037-179B-15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 07/795,323 PRIOR FILING DATE: 1994-09-27 NUMBER OF SEQ ID NOS: 21
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Darveau, Andre TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Zif268 zinc OTHER INFORMATION: finger 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                     ORGANISM: Artificial Sequence
                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Buckler, Alan J.
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Rose, Elise A.
Housman, David E.
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Haber, Daniel A.
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Darveau, Andre
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100.0%; Pred. No.
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0.043;
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Sequence 1, Application US/09714357

Patent No. 6708120

GENERAL INFORMATION:

APPLICANT: Mayo, Stephen L.

APPLICANT: Mayo, Stephen L.

APPLICANT: Dahiyat, Bassil I.

APPLICANT: Gordon, D. B.

APPLICANT: Street, Arthur

ITILE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN

FILE REFERENCE: A6535-3/RET/RMS/SJR

CURRENT APPLICATION NUMBER: US/09/714,357

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: 05/054,459

PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: 60/054,678

PRIOR APPLICATION NUMBER: 60/054,678

PRIOR APPLICATION NUMBER: 60/054,678

PRIOR APPLICATION NUMBER: 60/054,678

PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NO 1

SEQ ID NO 1

LENGTH: 28

TYPE: PRT

ORGANISM: Mouse

US-09-714-357-1
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Search completed: December 27, 2004, 20:31:04 Job time: 15.85 secs
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US-09-714-357-1
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                                                                                        14 RSDHLTT 20
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